# FIG. 1A

```
  1 GGATAAGCCT GGGGCCAGCA TGAGCCAGAG GGAGGGAAGT CTGGAAGACC
    CCTATTCGGA CCCCGGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG
  1                      M   S   Q   R   E   G   S   L   E   D   H

 51 ACCAGACTGA CTCCTCAATC TCATTCCTAC CCCATTTGGA GGCCAAGATC
    TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG
 12   Q   T   D   S   S   I   S   F   L   P   H   L   E   A   K   I

101 CGCCAGACAC ACAACCTTGC CCGCCTCCTG ACCAAATATG CAGAACAACT
    GCGGTCTGTG TGTTGGAACG GGCGGAGGAC TGGTTTATAC GTCTTGTTGA
 28 R   Q   T   H   N   L   A   R   L   L   T   K   Y   A   E   Q   L

151 TCTGGAGGAA TACGTGCAGC AACAGGGAGA GCCCTTTGGG CTGCCGGGCT
    AGACCTCCTT ATGCACGTCG TTGTCCCTCT CGGGAAACCC GACGGCCCGA
 45  L   E   E   Y   V   Q   Q   Q   G   E   P   F   G   L   P   G   F

201 TCTCACCACC GCGGCTGCCG CTGGCCGGCC TGAGTGGCCC GGCTCCGAGC
    AGAGTGGTGG CGCCGACGGC GACCGGCCGG ACTCACCGGG CCGAGGCTCG
 62   S   P   P   R   L   P   L   A   G   L   S   G   P   A   P   S

251 CATGCAGGGC TACCGGTGTC CGAGCGGCTG CGGCAGGATG CAGCCGCCCT
    GTACGTCCCG ATGGCCACAG GCTCGCCGAC GCCGTCCTAC GTCGGCGGGA
 78 H   A   G   L   P   V   S   E   R   L   R   Q   D   A   A   A   L

301 GAGTGTGCTG CCCGCGCTGT TGGATGCCGT CCGCCGCCGC CAGGCGGAGC
    CTCACACGAC GGGCGCGACA ACCTACGGCA GGCGGCGGCG GTCCGCCTCG
 95  S   V   L   P   A   L   L   D   A   V   R   R   R   Q   A   E   L

351 TGAACCCGCG CGCCCCGCGC CTGCTGCGGA GCCTGGAGGA CGCAGCCCGC
    ACTTGGGCGC GCGGGGCGCG GACGACGCCT CGGACCTCCT GCGTCGGGCG
112   N   P   R   A   P   R   L   L   R   S   L   E   D   A   A   R

401 CAGGTTCGGG CCCTGGGCGC CGCGGTGGAG ACAGTGCTGG CCGCGCTGGG
    GTCCAAGCCC GGGACCCGCG GCGCCACCTC TGTCACGACC GGCGCGACCC
128 Q   V   R   A   L   G   A   A   V   E   T   V   L   A   A   L   G

451 CGCTGCAGCC CGCGGGCCCG GGCCAGAGCC CGTCACCGTC GCCACCCTCT
    GCGACGTCGG GCGCCCGGGC CCGGTCTCGG GCAGTGGCAG CGGTGGGAGA
145 A   A   A   R   G   P   G   P   E   P   V   T   V   A   T   L   F

501 TCACGGCCAA CAGCACTGCA GGCATCTTCT CAGCCAAGGT GCTGGGGTTC
    AGTGCCGGTT GTCGTGACGT CCGTAGAAGA GTCGGTTCCA CGACCCCAAG
162   T   A   N   S   T   A   G   I   F   S   A   K   V   L   G   F

551 CACGTGTGCG GCCTCTATGG CGAGTGGGTG AGCCGCACAG AGGGCGACCT
    GTGCACACGC CGGAGATACC GCTCACCCAC TCGGCGTGTC TCCCGCTGGA
178 H   V   C   G   L   Y   G   E   W   V   S   R   T   E   G   D   L

601 GGGCCAGCTG GTGCCAGGGG GCGTCGCCTG AGAGTGAATA CTTTTTCTTG
    CCCGGTCGAC CACGGTCCCC CGCAGCGGAC TCTCACTTAT GAAAAAGAAC
195 G   Q   L   V   P   G   G   V   A   O
```

# FIG. 1B

```
 651 TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTTCT GTCTCTCCAT
     ATTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA

 701 CTGTGTCCTG TGTGTTCTTG GGCTGTCCCT ATCTTTCTGC ATTTGTGTGG
     GACACAGGAC ACACAAGAAC CCGACAGGGA TAGAAAGACG TAAACACACC

 751 TCTCTCTCTT CTGCTCTCCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT
     AGAGAGAGAA GACGAGAGGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA

 801 TTCTCGTTTT GTCTCTCTCC AGTCTTGAAC ACTTTTGTCT CCGAGAGGTC
     AAGAGCAAAA CAGAGAGAGG TCAGAACTTG TGAAAACAGA GGCTCTCCAG

 851 TCTTTTTGTT TCCTTGTCTC TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT
     AGAAAAACAA AGGAACAGAG AACCAAGAAA GAAACGAACG AACGAACGAA

 901 GCTTGCTTGT TGTTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG
     CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC

 951 GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG
     CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAC

1001 CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT
     GGAGGCTGAG GGTTAAAGGG GTAGACAGAG GGACACTAGG TATACCCATA

1051 GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT
     CACATTGGGA ATGAAACAGA GTACCTCCAC TGTTAAAAG AGGGAAGTCA

1101 TTCTTTGTTC TTTACTGACC AGAAAAGTGC CTACTTGTCC CCTGGTGGCA
     AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT

1151 AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCTTTGTA GGCAAATCCC
     TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG

1201 TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTCAATGGA
     AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT

1251 GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT
     CTCTCTTTCC GTCTTTTTGT AGAAATTTCT CAAAATAAAC TCTTATTTAA

1301 AATTTTTGTA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA
     TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTTGAA AATACTTTTT

1351 AA (polyA)
     TT
```

# FIG. 2

```
                 10        20        30        40        50
chf.781  MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQ
                       **        ***          *  *  **
humcntf           MAFTEHSPLTPHRRDLCSRSIWLARKIRSDLTALTESYVK
                       10        20        30        40


                 60        70        80        90       100
chf.781  QQGEPFGLPGFSPPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPAL
            **          *      *  *                ***       *        *
humcntf  HQGLNKNINLDSADGMPVA----STDQWSELTEAERLQENLQAYRTFHVL
            50            60        70        80


                110       120       130       140
chf.781  LD-AVRRRQAELNPRAPRLLRSLEDAARQVRALGAAVETVLAALGAAARG
            *        *       *              ** *       *          *
humcntf  LARLLEDQQVHFTPTEGDFHQAIHTLLLQVAAFAYQIEELMILLEYKIPR
            90          100       110       120       130


              150       160       170       180       190
chf.781  PGPEPVTVATLFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVP
                        *   *   *   *   *         *   *    **
humcntf  NEADGMPINV-----GDGGLFEKKLWGLKVLQELSQWTVRSIHDL-RFIS
            140             150       160       170       180


         200
chf.781  GGVAO

humcntf  SHQTGIPARGSHYIANNKKM
                      190       200
```
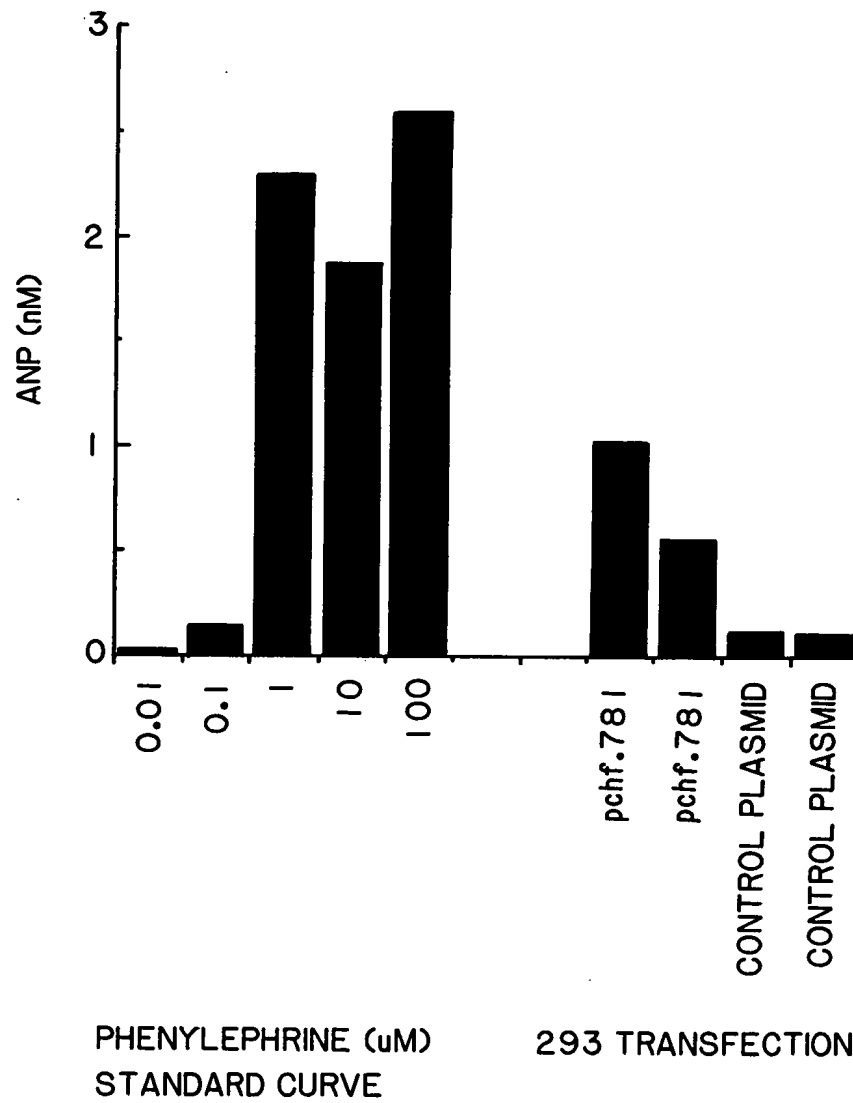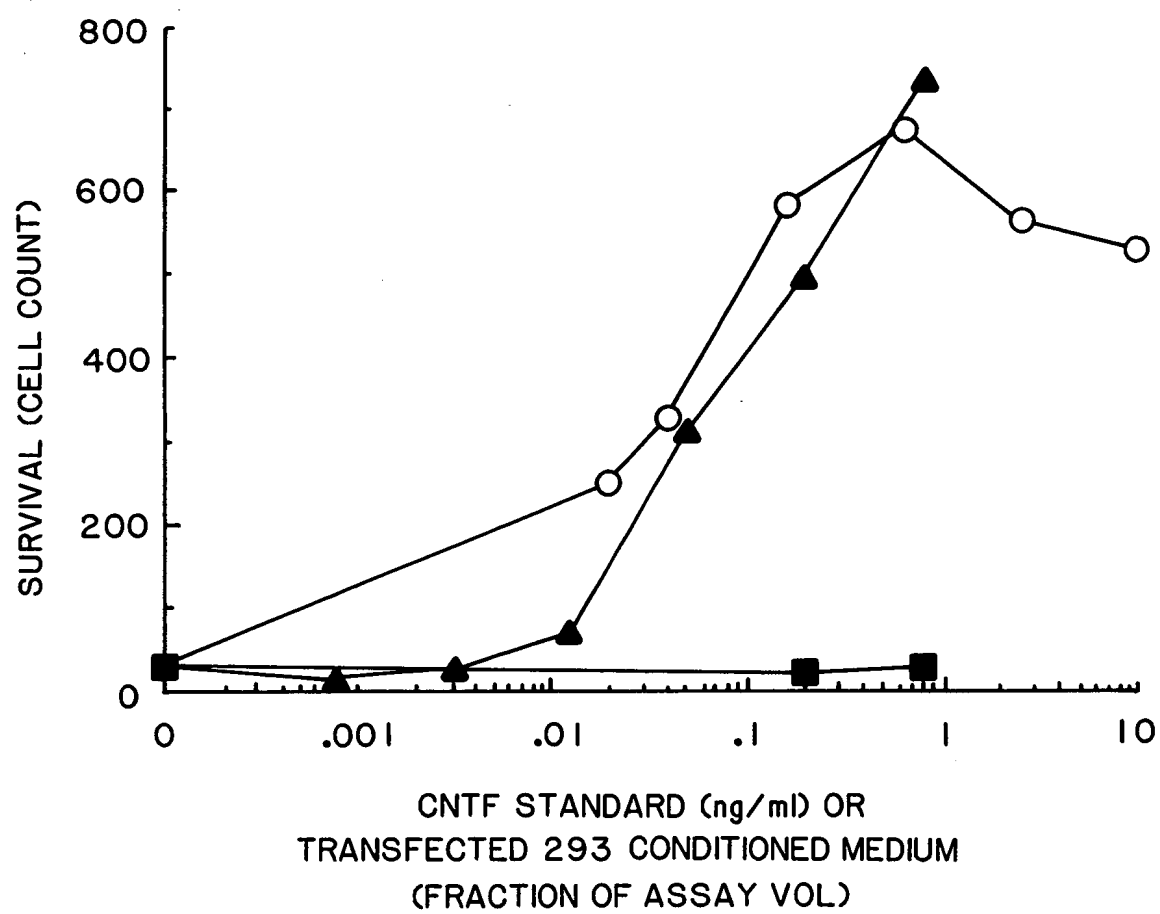
# FIG. 3

# FIG. 4



CNTF STANDARD (ng/ml) OR
TRANSFECTED 293 CONDITIONED MEDIUM
(FRACTION OF ASSAY VOL)

# FIG. 5A

```
  1   GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA
      CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT
  1                                      M  S  R    R  E  G


 51   AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT
      TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA
  7   S  L  E  D  P  Q  T  D  S  S    V  S  L  L  P  H  L


101   GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT
      CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA
 24   E  A  K   I  R  Q  T  H  S  L    A  H  L   L  T  K  Y


151   ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC
      TGCGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG
 41    A  E  Q   L  L  Q   E  Y  V  Q   L  Q  G   D  P  F


201   GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC
      CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG
 57   G  L  P  S  F  S  P  P  R  L    P  V  A  G   L  S  A


251   CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG
      GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC
 74   P  A  P   S  H  A  G  L  P  V  H  E  R   L  R  L  D


301   ACGCGGCGGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC
      TGCGCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG
 91    A  A  A   L  A  A   L  P  P  L   L  D  A   V  C  R


351   CGCCAGGCCG AGCTGAACCC GCGCGCGCCG CGCCTGCTGC GCCGCCTGGA
      GCGGTCCGGC TCGACTTGGG CGCGCGCGGC GCGGACGACG CGGCGGACCT
107   R  Q  A  E  L  N  P  R  A  P    R  L  L  R  R  L  E


401   GGACGCGGCG CGCCAGGCCC GGGCCCTGGG CGCCGCCGTG GAGGCCTTGC
      CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG
124   D  A  A   R  Q  A  R   A  L  G   A  A  V   E  A  L  L


451   TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCGGGCCGA GCCCCCCGCC
      ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGCCCGGCT CGGGGGGCGG
141   A  A  L   G  A  A   N  R  G  P   R  A  E   P  P  A
```

# FIG. 5B

```
 501   GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT
       CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCCACGA
 157    A  T  A  S   A  A  S   A  T  G   V  F  P  A   K  V  L


 551   GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG
       CCCCGAGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC
 174     G  L  R   V  C  G  L   Y  R  E   W  L  S   R  T  E  G


 601   GCGACCTGGG CCAGCTGCTG CCCGGGGGCT CGGCCTGAGC GCCGCGGGGC
       CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG
 191     D  L  G   Q  L  L   P  G  G  S   A  O


 651   AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT
       TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GGCGAAGAAA


 701   GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC
       CAGAAAGAGA CGGCGACAGC CACAGACAGA CAGACGAGAA TCGACAGAGG


 751   ATTGCCTCGG CCTTCTTTGC TTTTTGTGGG GGAGAGGGGA GGGGACGGGC
       TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCCT CCCCTGCCCG


 801   AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC
       TCCCAGAGAC AGCGGGTCCG ACCCCACGTC ACCGCGCTAG GGTCGTGACG


 851   AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC
       TCGGAGTTGG AGGACCCGAG TTCGGTAGGA AGGCGGAGTC GAAGGGGTCG


 901   AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTTAA
       TCGACCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAATAAATT


 951   TTTTTTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAACT
       AAAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA


1001   CCGGGGCTCA AGCGATCC
       GGCCCCGAGT TCGCTAGG
```

# FIG. 6

```
humct1     1  MSRREGSLEDPQTDSSVSLLPHLEAKIRQTHSLAHLLTKYAEQLLQEYVQLQG
              ** ******* ***** * ************ ** ********* **** **
chf.781    1  MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQQQG


humct1    54  DPFGLPSFSPPRLPVAGLSAPAPSHAGLPVHERLRLDAAALAALPPLLDAVCR
              **** ******* **** ********** **** *****   ** ***** *
chf.781   54  EPFGLPGFSPPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPALLDAVRR


humct1   107  RQAELNPRAPRLLRRLEDAARQARALGAAVEALLAALGAANRGPRAEPPAATA
              ************* ******* ******* *******   ******* ***   **
chf.781  107  RQAELNPRAPRLLRSLEDAARQVRALGAAVETVLAALGAAARGPGPEPVTVAT


humct1   160  --SAASATGVFPAKVLGLRVCGLYREWLSRTEGDLGQLLPGGSA
              *  *   * * ***** ***** ** ********** *** *
chf.781  160  LFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVPGGVA
```